

SEQUENCE LISTING

<110> Ruan, Yong-Ling
 Furbank, Robert T.
 Danny, Llewellyn J.

<120> Modification of sucrose synthase gene expression in plant tissue and uses therefor

<130> GHSUSY WO1

<150> 60/251852
 <151> 2000-12-08

<160> 6

<170> PatentIn version 3.1

<210> 1
 <211> 2625
 <212> DNA
 <213> Gossypium hirsutum

<220>
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 <223> n = any nucleotide (a,g,c,t)

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 Met Ala Glu Arg Ala Leu Thr Arg Val His Ser Leu Arg Glu Arg Leu
 1 5 10 15

gat gag acc ctt ctt gct cac agg aac gag att ttg gcc ttg ctc tca 96
 Asp Glu Thr Leu Leu Ala His Arg Asn Glu Ile Leu Ala Leu Leu Ser
 20 25 30

agg atc gag ggc aaa gga aaa gga att ctg caa cac cat caa att att 144
 Arg Ile Glu Gly Lys Gly Lys Gly Ile Leu Gln His His Gln Ile Ile
 35 40 45

cta gag ttt gaa gct atc cct gaa gag aac aga aag aag ctc gct aat 192
 Leu Glu Phe Glu Ala Ile Pro Glu Glu Asn Arg Lys Lys Leu Ala Asn
 50 55 60

ggt gca ttt ttt gaa gta ttg aag gct agt cag gaa gcg atc gtg ttg 240
 Gly Ala Phe Phe Glu Val Leu Lys Ala Ser Gln Glu Ala Ile Val Leu
 65 70 75 80

cct cca tgg gtt gca ctt gct gtt cgt cca agg cct ggt gtt tgg gag 288
 Pro Pro Trp Val Ala Leu Ala Val Arg Pro Arg Pro Gly Val Trp Glu

85	90	95	
tac att aga gtg aat gtt cac gcc ctt gtt gag gaa ctc act gtt Tyr Ile Arg Val Asn Val His Ala Leu Val Val Glu Glu Leu Thr Val 100	105	110	336
gct gag tat ctc cac ttc aag gaa gag ctt gtt gat gga agt tca aat Ala Glu Tyr Leu His Phe Lys Glu Glu Leu Val Asp Gly Ser Ser Asn 115	120	125	384
gga aac ttt gtt ttg gaa ttg gat ttt gag ccc ttc aac tca tca ttc Gly Asn Phe Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ser Ser Phe 130	135	140	432
ccc cgc cca act ctt tca aaa tcc att ggt aat ggt gtg gag ttc cta Pro Arg Pro Thr Leu Ser Lys Ser Ile Gly Asn Gly Val Glu Phe Leu 145	150	155	480
aat cgt cac ctt tcg gca aaa ttg ttc cat gac aag gag agc atg cac Asn Arg His Leu Ser Ala Lys Leu Phe His Asp Lys Glu Ser Met His 165	170	175	528
cct ttg ctc gaa ttc ctc aga gtc cat tgt cac aag ggc aag aac atg Pro Leu Leu Glu Phe Leu Arg Val His Cys His Lys Gly Lys Asn Met 180	185	190	576
atg ttg aat gac aga att cag aac ttg aat gct ctt caa cat gtt ttg Met Leu Asn Asp Arg Ile Gln Asn Leu Asn Ala Leu Gln His Val Leu 195	200	205	624
agg aaa gca gag gag tat ctt ggt acc cta cct cct gag aca cca tgt Arg Lys Ala Glu Glu Tyr Leu Gly Thr Leu Pro Pro Glu Thr Pro Cys 210	215	220	672
gcc gaa ttc gaa cac cgg ttc cag gaa atc ggt ttg gaa aga ggt tgg Ala Glu Phe Glu His Arg Phe Gln Glu Ile Gly Leu Glu Arg Gly Trp 225	230	235	720
ggt gac acc gca gaa cgc gtg ctc gag atg atc caa ctc ctt ttg gat Gly Asp Thr Ala Glu Arg Val Leu Glu Met Ile Gln Leu Leu Leu Asp 245	250	255	768
ttt ctt gag gca act gat cct tgc acc ctt gag aag ttc ctt ggg aga Leu Leu Glu Ala Thr Asp Pro Cys Thr Leu Glu Lys Phe Leu Gly Arg 260	265	270	816
atc ccc atg gtg ttc aat gtt gtg att ctc act ccc cac gga tac ttc Ile Pro Met Val Phe Asn Val Val Ile Leu Thr Pro His Gly Tyr Phe 275	280	285	864
gct caa gac aat gtt ttg ggg tat ccc gac acc ggt ggg cag gtt gtt Ala Gln Asp Asn Val Leu Glu Tyr Pro Asp Thr Gly Gly Gln Val Val 290	295	300	912
tac atc ttg gat caa gtc cga gct ttg gag aat gag atg ctc ctc cgt Tyr Ile Leu Asp Gln Val Arg Ala Leu Glu Asn Glu Met Leu Leu Arg 305	310	315	960

ata aag caa caa gga ctc aac atc acc cct cga atc ctc att att act Ile Lys Gln Gln Gly Leu Asn Ile Thr Pro Arg Ile Leu Ile Thr 325 330 335	1008
aga ctt ctt cct gat gct gtc gga aca aca tgc ggt caa cga ctt gag Arg Leu Leu Pro Asp Ala Val Gly Thr Thr Cys Gly Gln Arg Leu Glu 340 345 350	1056
aaa gta tac gga aca gag cac tcg gat att ctt cga gta ccc ttc aga Lys Val Tyr Gly Thr Glu His Ser Asp Ile Leu Arg Val Pro Phe Arg 355 360 365	1104
aca gaa aag gga att gtt cga aaa tgg atc tca aga ttt gaa aaa gtc Thr Glu Lys Gly Ile Val Arg Lys Trp Ile Ser Arg Phe Glu Lys Val 370 375 380	1152
tgg cca tac ttg gaa acc tac aca gag gat gtt gct cat gaa atc tcc Trp Pro Tyr Leu Glu Thr Tyr Thr Glu Asp Val Ala His Glu Ile Ser 385 390 395 400	1200
aaa gag ttg cac ggc acg cca gat ctg atc atc gga aac nac agc gac Lys Glu Leu His Gly Thr Pro Asp Leu Ile Ile Gly Asn Xaa Ser Asp 405 410 415	1248
ggc aat atc gtc gcc tcc ttg ctc gca cat aaa tta ggt gtc aca cag Gly Asn Ile Val Ala Ser Leu Leu Ala His Lys Leu Gly Val Thr Gln 420 425 430	1296
tgc acc atc gcc cat gct ttg gag aag aca aaa tat cca gat tca gat Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asp Ser Asp 435 440 445	1344
atc tat ttg aag aag ctt gaa gac aaa tac cat ttc tct tgc caa ttt Ile Tyr Trp Lys Lys Leu Glu Asp Lys Tyr His Phe Ser Cys Gln Phe 450 455 460	1392
aca gct gat ctt ttt gca atg aac cat aca gat ttc atc atc acc agt Thr Ala Asp Leu Phe Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser 465 470 475 480	1440
act ttc cag gaa att gca gga agc aag gac act gtt ggt caa tac gag Thr Phe Gln Glu Ile Ala Gly Ser Lys Asp Thr Val Gly Gln Tyr Glu 485 490 495	1488
agc cac act gct ttc act ctt cct ggt ctc tac cgt gtt gta cat ggt Ser His Thr Ala Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly 500 505 510	1536
atc gat gtg ttt gat ccc aaa ttc aac att gtt tcc cct ggt gct gat Ile Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp 515 520 525	1584
atg gag ata tac ttc cct tac acc gaa gag aag cgg agg ttg aag cat Met Glu Ile Tyr Phe Pro Tyr Thr Glu Glu Lys Arg Arg Leu Lys His 530 535 540	1632
ttc cat cct gag atc gaa gac ctt ctt tac acc aaa gtt gag aat gaa Phe His Pro Glu Ile Glu Asp Leu Leu Tyr Thr Lys Val Glu Asn Glu	1680

545	550	555	560	
gaa cac tta tgt gtg ctc aat gac cgc aac aag cca att ctg ttc aca				1728
Glu His Leu Cys Val Leu Asn Asp Arg Asn Lys Pro Ile Leu Phe Thr				
565	570	575		
atg cca agg ctt gat cgt gtc aag aac tta acc gga ctc gtc gag tgg				1776
Met Pro Arg Leu Asp Arg Val Lys Asn Leu Thr Gly Leu Val Glu Trp				
580	585	590		
tgc ggc aag aac cca aag ttg cgt gag ttg gct aac ctc gta gtt gta				1824
Cys Gly Lys Asn Pro Lys Leu Arg Glu Leu Ala Asn Leu Val Val Val				
595	600	605		
ggt ggt gat agg cga aag gaa tct aaa gat ttg gaa gag aag gct gaa				1872
Gly Gly Asp Arg Arg Lys Glu Ser Lys Asp Leu Glu Glu Lys Ala Glu				
610	615	620		
atg aag aaa atg ttt gag ctg atc gac aag tac aac ttg aac ggc caa				1920
Met Lys Met Phe Glu Leu Ile Asp Lys Tyr Asn Leu Asn Gly Gln				
625	630	635	640	
ttc aga tgg ata tca tct caa atg aac aga atc cga aat gtt gaa ctt				1968
Phe Arg Trp Ile Ser Ser Gln Met Asn Arg Ile Arg Asn Val Glu Leu				
645	650	655		
ttac cga tac att tgc gac acg aaa ggt gcc ttt gta cag cct gca ttg				2016
Tyr Arg Tyr Ile Cys Asp Thr Lys Gly Ala Phe Val Gln Pro Ala Leu				
660	665	670		
ttat gaa gcc ttt gga ttg aca gtt gtg gag gca atg act tgc ggt ttg				2064
Tyr Glu Ala Phe Gly Leu Thr Val Val Glu Ala Met Thr Cys Gly Leu				
675	680	685		
ccca aca ttc gca acc tgt aac ggt gga cca gcc gag att att gtc cat				2112
Pro Thr Phe Ala Thr Cys Asn Gly Gly Pro Ala Glu Ile Ile Val His				
690	695	700		
ggg aaa tct ggt ttc aac att gat cct tac cat ggt gat caa gct gct				2160
Gly Lys Ser Gly Phe Asn Ile Asp Pro Tyr His Gly Asp Gln Ala Ala				
705	710	715	720	
gac ata ctc gtc gat ttc ttt gaa aag tgt aag aaa gat cca tct cac				2208
Asp Ile Leu Val Asp Phe Glu Lys Cys Lys Lys Asp Pro Ser His				
725	730	735		
tgg gat aag atc tcc caa gga ggc ttg aaa cga ata gag gag aag tat				2256
Trp Asp Lys Ile Ser Gln Gly Gly Leu Lys Arg Ile Glu Glu Lys Tyr				
740	745	750		
aca tgg aag att tac tcg gag aga cta ttg acc ctg aca gga gtg tat				2304
Thr Trp Lys Ile Tyr Ser Glu Arg Leu Leu Thr Leu Thr Gly Val Tyr				
755	760	765		
gga ttc tgg aag cat gtt tcc aac ctt gaa cgc cgt gag agt cgt cgt				2352
Gly Phe Trp Lys His Val Ser Asn Leu Glu Arg Arg Glu Ser Arg Arg				
770	775	780		

tac ctt gag atg ttt tat gct ctt aag tac cgt aag ctg gct gaa tca	2400
Tyr Leu Glu Met Phe Tyr Ala Leu Lys Tyr Arg Lys Leu Ala Glu Ser	
785 790 795 800	
gtt cca ttg gca gag gag taa att gaa cct gtt aaa taa cat tgg gcc	2448
Val Pro Leu Ala Glu Glu Ile Glu Pro Val Lys His Trp Ala	
805 810	
ggt ttt tct tgg aga ata ata ttc tgt ttt gta att tca att gga gaa	2496
Gly Phe Ser Trp Arg Ile Ile Phe Cys Phe Val Ile Ser Ile Gly Glu	
815 820 825 830	
gct cct ttg tat ttc atc ttg tct ttt cct ttt ttc gcc ggc	2544
Ala Pro Leu Tyr Phe Ile Leu Ser Phe Pro Phe Pro Phe Ala Gly	
835 840 845	
att gtt tga aca tgg ggt tgt gcg ccc gtc aat tcc agt taa ata tgg	2592
Ile Val Thr Trp Gly Cys Ala Pro Val Asn Ser Ser Ile Trp	
850 855 860	

tga ctt ttg ttt ttc aaa aaa aaa aaa aaa aaa	2625
Leu Leu Phe Phe Lys Lys Lys Lys Lys Lys	
865 870	

<210> 2
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 <212> PRT
 <213> Gossypium hirsutum

<220>
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 <222> (414)..(414)
 <223> The 'Xaa' at location 414 stands for Asn, Asp, His, or Tyr.

<220>
 <221> misc_feature
 <222> (1240)..(1240)
 <223> n = any nucleotide (a,g,c,t)

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Met Ala Glu Arg Ala Leu Thr Arg Val His Ser Leu Arg Glu Arg Leu	
1 5 10 15	

Asp Glu Thr Leu Leu Ala His Arg Asn Glu Ile Leu Ala Leu Leu Ser	
20 25 30	

Arg Ile Glu Gly Lys Gly Lys Gly Ile Leu Gln His His Gln Ile Ile	
35 40 45	

Leu Glu Phe Glu Ala Ile Pro Glu Glu Asn Arg Lys Lys Leu Ala Asn	
50 55 60	

Gly Ala Phe Phe Glu Val Leu Lys Ala Ser Gln Glu Ala Ile Val Leu
65 70 75 80

Pro Pro Trp Val Ala Leu Ala Val Arg Pro Arg Pro Gly Val Trp Glu
85 90 95

Tyr Ile Arg Val Asn Val His Ala Leu Val Val Glu Glu Leu Thr Val
100 105 110

Ala Glu Tyr Leu His Phe Lys Glu Glu Leu Val Asp Gly Ser Ser Asn
115 120 125

Gly Asn Phe Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ser Ser Phe
130 135 140

Pro Arg Pro Thr Leu Ser Lys Ser Ile Gly Asn Gly Val Glu Phe Leu
145 150 155 160

Asn Arg His Leu Ser Ala Lys Leu Phe His Asp Lys Glu Ser Met His
165 170 175

Pro Leu Leu Glu Phe Leu Arg Val His Cys His Lys Gly Lys Asn Met
180 185 190

Met Leu Asn Asp Arg Ile Gln Asn Leu Asn Ala Leu Gln His Val Leu
195 200 205

Arg Lys Ala Glu Glu Tyr Leu Gly Thr Leu Pro Pro Glu Thr Pro Cys
210 215 220

Ala Glu Phe Glu His Arg Phe Gln Glu Ile Gly Leu Glu Arg Gly Trp
225 230 235 240

Gly Asp Thr Ala Glu Arg Val Leu Glu Met Ile Gln Leu Leu Leu Asp
245 250 255

Leu Leu Glu Ala Thr Asp Pro Cys Thr Leu Glu Lys Phe Leu Gly Arg
260 265 270

Ile Pro Met Val Phe Asn Val Val Ile Leu Thr Pro His Gly Tyr Phe
275 280 285

Ala Gln Asp Asn Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val
290 295 300

Tyr Ile Leu Asp Gln Val Arg Ala Leu Glu Asn Glu Met Leu Leu Arg
305 310 315 320

Ile Lys Gln Gln Gly Leu Asn Ile Thr Pro Arg Ile Leu Ile Ile Thr
325 330 335

Arg Leu Leu Pro Asp Ala Val Gly Thr Thr Cys Gly Gln Arg Leu Glu
340 345 350

Lys Val Tyr Gly Thr Glu His Ser Asp Ile Leu Arg Val Pro Phe Arg
355 360 365

Thr Glu Lys Gly Ile Val Arg Lys Trp Ile Ser Arg Phe Glu Lys Val
370 375 380

Trp Pro Tyr Leu Glu Thr Tyr Thr Glu Asp Val Ala His Glu Ile Ser
385 390 395 400

Lys Glu Leu His Gly Thr Pro Asp Leu Ile Ile Gly Asn Xaa Ser Asp
405 410 415

Gly Asn Ile Val Ala Ser Leu Leu Ala His Lys Leu Gly Val Thr Gln
420 425 430

Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asp Ser Asp
435 440 445

Ile Tyr Trp Lys Lys Leu Glu Asp Lys Tyr His Phe Ser Cys Gln Phe
450 455 460

Thr Ala Asp Leu Phe Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser
465 470 475 480

Thr Phe Gln Glu Ile Ala Gly Ser Lys Asp Thr Val Gly Gln Tyr Glu
485 490 495

Ser His Thr Ala Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly
500 505 510

Ile Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp
515 520 525

Met Glu Ile Tyr Phe Pro Tyr Thr Glu Glu Lys Arg Arg Leu Lys His
530 535 540

Phe His Pro Glu Ile Glu Asp Leu Leu Tyr Thr Lys Val Glu Asn Glu
545 550 555 560

Glu His Leu Cys Val Leu Asn Asp Arg Asn Lys Pro Ile Leu Phe Thr
565 570 575

Met Pro Arg Leu Asp Arg Val Lys Asn Leu Thr Gly Leu Val Glu Trp
580 585 590

Cys Gly Lys Asn Pro Lys Leu Arg Glu Leu Ala Asn Leu Val Val Val
595 600 605

Gly Gly Asp Arg Arg Lys Glu Ser Lys Asp Leu Glu Glu Lys Ala Glu
610 615 620

Met Lys Lys Met Phe Glu Leu Ile Asp Lys Tyr Asn Leu Asn Gly Gln
625 630 635 640

Phe Arg Trp Ile Ser Ser Gln Met Asn Arg Ile Arg Asn Val Glu Leu
645 650 655

Tyr Arg Tyr Ile Cys Asp Thr Lys Gly Ala Phe Val Gln Pro Ala Leu
660 665 670

Tyr Glu Ala Phe Gly Leu Thr Val Val Glu Ala Met Thr Cys Gly Leu
675 680 685

Pro Thr Phe Ala Thr Cys Asn Gly Gly Pro Ala Glu Ile Ile Val His
690 695 700

Gly Lys Ser Gly Phe Asn Ile Asp Pro Tyr His Gly Asp Gln Ala Ala
705 710 715 720

Asp Ile Leu Val Asp Phe Phe Glu Lys Cys Lys Lys Asp Pro Ser His
725 730 735

Trp Asp Lys Ile Ser Gln Gly Gly Leu Lys Arg Ile Glu Glu Lys Tyr
740 745 750

Thr Trp Lys Ile Tyr Ser Glu Arg Leu Leu Thr Leu Thr Gly Val Tyr
755 760 765

Gly Phe Trp Lys His Val Ser Asn Leu Glu Arg Arg Glu Ser Arg Arg
770 775 780

Tyr Leu Glu Met Phe Tyr Ala Leu Lys Tyr Arg Lys Leu Ala Glu Ser
785 790 795 800

Val Pro Leu Ala Glu Glu
805

<210> 3
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<212> PRT
<213> Gossypium hirsutum

<220>
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<223> n = any nucleotide (a,g,c,t)

<400> 3

Ile Glu Pro Val Lys
1 5

<210> 4
<211> 37
<212> PRT
<213> Gossypium hirsutum

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His Trp Ala Gly Phe Ser Trp Arg Ile Ile Phe Cys Phe Val Ile Ser
1 5 10 15

Ile Gly Glu Ala Pro Leu Tyr Phe Ile Leu Ser Phe Pro Phe Pro Phe
20 25 30

Phe Ala Gly Ile Val
35

<210> 5
<211> 10
<212> PRT
<213> Gossypium hirsutum

<220>
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<223> n = any nucleotide (a,g,c,t)

<400> 5

Thr Trp Gly Cys Ala Pro Val Asn Ser Ser
1 5 10

<210> 6
<211> 10
<212> PRT
<213> Gossypium hirsutum

<220>
<221> misc_feature
<222> (1240)..(1240)
<223> n = any nucleotide (a,g,c,t)

<400> 6

Leu Leu Phe Phe Lys Lys Lys Lys Lys Lys
1 5 10